Mixed models of large pedigrees in genetic association studies

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Standard approaches in genetic linkage and association analysis of data from large pedigrees have limited ability to handle covariates, which are important for studying their main effects and interactions with genetic markers. We desribed mixed models appropriate for analyzing such data. In particular, our motivating example was a simulated data distributed through the Genetic Analysis Workshop (GAW17) for which three types of mixed models have been fitted: a linear model of quantitative trait, a logistic model of binary trait, and a Cox model of binary trait and age at onset. The relevant functions `lmekin` for linear model and `coxme` for Cox model are from the *R* package **kinship** and able to accommodate kinship and identity-by-descent (IBD) information, while function `pedigreemm` from the *R* package **pedigreemm** allows for Gaussian, binary and Poisson responses with kinship but not IBD information. We compared these with procedures in *SAS*. We found that avaibility of a good IBD information can be useful for positional cloning and fine mapping in genome-wide association studies involving single nucleotide polymorphisms. We believe that our work will be of practical use to researchers in their analysis of pedigree data.

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